

```
10      20      30      40      50      60
CATCAATCAAT AATCTACAGT AACTGATGG CAGCGGTCCA ACTGCCAATC ATTTTGGCCA

70      80      90      100     110     120
CGTCATTAT GACGCAACGA CGGCGAGCGT GCGTGCTGA CGTAACGTG GGGCGGAGCG

130     140     150     160     170     180
CGTCGGGAG GCGGCGGCGC TGGGCGGGC TGAGGGCGGC GGGGGCGGCG CGCGGGGGCGG

190     200     210     220     230     240
CGCGCGGGC GGGGCGAGG GCGGAGTCC GCACCCGCTA CGTCATTTC AGACATTTT

250     260     270     280     290     300
TAGCAAAATT GCGCCTTTTG CAAGCATTTT TCTCACATTT CAGGTATTTA GAGGGCGGAT

310     320     330     340     350     360
TTTTGGTGTT CGTACTTCCG TGTCACATAG TTCACTGTCA ATCTTCATTA CGGCTTAGAC

370     380     390     400     410     420
AAATTTTCGG CGTCCTTTTCC GGGTTTATGT CCCCAGTCAC CTTTATGACT GTGTGAAACA

430     440     450     460     470     480
CACCTGCCCA TTGTTTACCC TTGGTCAGTT TTTTCGTCTC CTAGGGTGGG AACATCAAGA
```

FIG. 1A

#2

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490      500      510      520      530      540
ACAAATTGCG CGAGTAATTG TGCACCTTTT TCCGCGGTAG GACTGCGTTT CACACGTAGA

550      560      570      580      590      600
CAGACTTTT CTCATTTTCT CACACTCCGT CGTCCGCTTC AGAGCTCTGC GTCTTCGCTG

610      620      630      640      650
CCACC ATG AAG TAC CTG GTC CTC GTT CTC AAC GAC GGC ATG AGT CGA ATT GAA
Met Lys Tyr Leu Val Leu Val Leu Asn Asp Gly Met Ser Arg Ile Glu

660      670      680      690      700
AAA GCT CTC CTG TGC AGC GAT GGT GAG GTG GAT TTA GAG TGT CAT GAG GTA
Lys Ala Leu Leu Cys Ser Asp Gly Glu Val Asp Leu Glu Cys His Glu Val

710      720      730      740      750
CTT CCC CCT TCT CCC GCG CCT GTC CCC GCT TCT GTG TCA CCC GTG AGG AGT
Leu Pro Pro Ser Pro Ala Pro Val Pro Ala Ser Val Ser Pro Val Arg Ser

760      770      780      790      800
CCT CCT CCT CTG TCT CCG GTG TTT CCT CCG TCT CCG CCA GCC CCG CTT GTG
Pro Pro Pro Leu Ser Pro Val Phe Pro Pro Ser Pro Pro Ala Pro Leu Val

810      820      830      840
AAT CCA GAG GCG AGT TCG CTG CTG CAG CAG TAT CGG AGA GAG CTG TTA GAG
Asn Pro Glu Ala Ser Ser Leu Leu Gln Tyr Arg Arg Glu Leu Leu Glu
```

FIG. 1B

860 870 880 890 900
AGG AGC CTG CTC CGA ACG GCC GAA GGT CAG CAG CGT GCA GTG TGT CCA TGT
Arg Ser Leu Leu Arg Thr Ala Glu Gly Gln Arg Ala Val Cys Pro Cys
910 920 930 940 950
GAG CGG TTG CCC GTG GAA GAG GAT GAG TGT CTG AAT GCC GTA AAT TTG CTG
Glu Arg Leu Pro Val Glu Glu Asp Glu Cys Leu Asn Ala Val Asn Leu Leu
960 970 980 990 1000 1010
TTT CCT GAT CCC TGG CTA AAT GCA GCT GAA AAT GGG GGT GAT ATT TTT AAG
Phe Pro Asp Pro Trp Leu Asn Ala Ala Glu Asn Gly Gly Asp Ile Phe Lys
1020 1030 1040 1050 1060
TCT CCG GCT ATG TCT CCA GAA CCG TGG ATA GAT TTG TCT AGC TAC GAT AGC
Ser Pro Ala Met Ser Pro Glu Pro Trp Ile Asp Leu Ser Ser Tyr Asp Ser
1070 1080 1090 1100 1110
GAT GTA GAA GAG GTG ACT AGT CAC TTT TTT CTG GAT TGC CCT GAA GAC CCC
Asp Val Glu Glu Val Thr Ser Ser His Phe Leu Asp Cys Pro Glu Asp Pro
1120 1130 1140 1150 1160
AGT CCG GAG TGT TCA TCT TGT GGG TTT CAT CAG GCT CAA AGC GGA ATT CCA
Ser Arg Glu Cys Ser Ser Cys Gly Phe His Gln Ala Gln Ser Gly Ile Pro

FIG. 1C

1170 1180 1190 1200 1210
GGC ATT ATG TGC AGT TTG TGC TAC ATG CGC CAA ACC TAC CAT TGC ATC TAT
Gly Ile Met Cys Ser Leu Cys Tyr Met Arg Gln Thr Tyr His Cys Ile Tyr

1220 1230 1240 1250 1260 1270
A GTAAG TACATTCTGT AAAAGAACAT CTTCGGTGATT TCTAGGTATT GTTTAGGGAT
S

1280 1290 1300 1310 1320 1330
TAACTGGGTG GAGTGATCTT AATCCGGCAT AACCAATAC ATGTTTTCAC AGJGT CCA GTT
er Pro Val

1340 1350 1360 1370 1380 1390
TCT GAA GAG GAA ATG TGAGT CATGTTGACT TTGGCGGC A AGAGGAAATG TGAGTCATGT
Ser Glu Glu Met End

1400 1410 1420 1430 1440 1450
TGACTTTGGC GCGCCCTACG GTGACTTTAA AGCAATTGA GGATCACTTT TTTGTTAGTC

1460 1470 1480 1490 1500
GCTATAAAGT AGTCACGGAG TCTTC ATG GAT CAC TTA AGC GTT CTT TTG GAT TTG
Met Asp His Leu Ser Val Leu Leu Asp Leu

1510 1520 1530 1540 1550
AAG CTG CTT CGC TCT ATC GTA GCG GGG GCT TCA AAT CGC ACT GGA GTG TGG
Lys Leu Leu Arg Ser Ile Val Ala Gly Ala Ser Asn Arg Thr Gly Val Trp

FIG. ID

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1560      1570      1580      1590      1600
AAG AGG CCG CTG TGG CTG GGA CGC CTG ACT CAA CTG GTC CAT GAT ACC TGC
Lys Arg Arg Leu Trp Leu Gly Arg Leu Thr Gln Leu Val His Asp Thr Cys

1610      1620      1630      1640      1650
GTA GAG AAC GAG AGC ATA TTT CTC AAT TCT CTG CCA GGG AAT GAA GCT TTT
Val Glu Asn Glu Ser Ile Phe Leu Asn Ser Leu Pro Gly Asn Glu Ala Phe

1660      1670      1680      1690      1700
TTA AGG TTG CTT CGG AGC GGC TAT TTT GAA GTG TTT GAC GTG TTT GTG GTG
Leu Arg Leu Leu Arg Ser Gly Tyr Phe Glu Val Phe Asp Val Phe Val Val

1710      1720      1730      1740      1750      1760
CCT GAG CTG CAT CTG GAC ACT CCG GGT CGA GTG GTC GCC GCT CTT GCT CTG
Pro Glu Leu His Leu Asp Thr Pro Gly Arg Val Val Ala Ala Leu Ala Leu

1770      1780      1790      1800      1810
CTG GTG TTC ATC CTC AAC GAT TTA GAC GCT AAT TCT GCT TCT TCA GGC TTT
Leu Val Phe Ile Leu Asn Asp Leu Asp Ala Asn Ser Ala Ser Ser Gly Phe

1820      1830      1840      1850      1860
GAT TCA GGT TTT CTC GTG GAC CGT CTC CTC TGC GTG CCG CTA TGG CTG AAG GCC
Asp Ser Gly Phe Leu Val Asp Arg Leu Cys Val Pro Leu Trp Leu Lys Ala
Met Ala Glu Gly
  
```

FIG. 1E

1870 1880 1890 1900 1910
AGG GCG TTC AAG ATC ACC CAG AGC TCC AGG AGC ACT TCG CAG CCT TCC TCG
Arg Ala Phe Lys Ile Thr Gln Ser Ser Arg Ser Thr Ser Gln Pro Ser Ser
Gln Gly Val Gln Asp His Pro Glu Leu Gln Glu His Phe Ala Ala Phe Leu

1920 1930 1940 1950 1960
TCG CCC GAC AAG ACC CAG ACT ACC AGC CAG TA GAC GGG GAC AGC CCA
Ser Pro Asp Lys Thr Thr Gln Thr Thr Ser Gln End
Val Ala Arg Gln Asp Asp Pro Asp Tyr Gln Pro Val Asp Gly Asp Ser Pro

1970 1980 1990 2000 2010
CCC CGG GCT AGC CTG GAG GAG GCT GAA CAG AGC AGC ACT CGT TTC GAG CAC
Pro Arg Ala Ser Leu Glu Glu Ala Glu Gln Ser Ser Thr Arg Phe Glu His

2020 2030 2040 2050 2060
ATC AGT TAC CGA GAC GTG GTG GAT GAC TTC AAT AGA TGC CAT GAT GTT TTT
Ile Ser Tyr Arg Asp Val Val Asp Asp Phe Asn Arg Cys His Asp Val Phe

2070 2080 2090 2100 2110
TAT GAG AGG TAC AGT TTT GAG GAC ATA AAG AGC TAC GAG GCT TTG CCT GAG
Tyr Glu Arg Tyr Ser Phe Glu Asp Ile Lys Ser Tyr Glu Ala Leu Pro Glu

FIG. 1F

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2120      2130      2140      2150      2160
GAC AAT TTG GAG CAG CTC ATA GCT ATG CAT GCT AAA ATC AAG CTG CTG CCC
Asp Asn Leu Glu Gln Leu Ile Ala Met His Ala Lys Ile Lys Leu Leu Pro

2170      2180      2190      2200      2210
GGT CGG GAG TAT GAG TTG ACT CAA CCT TTG AAC ATA ACA TCT TGC GCC TAT
Gly Arg Glu Tyr Glu Leu Thr Gln Pro Leu Asn Ile Thr Ser Cys Ala Tyr

2220      2230      2240      2250      2260
GTG CTC GGA AAT GGG GCT ACT ATT AGG GTA ACA GGG GAA GCC TCC CCG GCT
Val Leu Gly Asn Gly Ala Thr Ile Arg Val Thr Gly Glu Ala Ser Pro Ala

2270      2280      2290      2300      2310      2320
ATT AGA GTG GGG GCC ATG GCC GTG GGT CCG TGT GTA ACA GGA ATG ACT GGG
Ile Arg Val Gly Ala Met Ala Val Gly Pro Cys Val Thr Gly Met Thr Gly

2330      2340      2350      2360      2370
GTG ACT TTT GTG AAT TGT AGG TTT GAG AGA GAG TCA ACA ATT AGG GGG TCC
Val Thr Phe Val Asn Cys Arg Phe Glu Arg Glu Ser Thr Ile Arg Gly Ser

2380      2390      2400      2410      2420
CTG ATA CGA GCT TCA ACT CAC GTG CTG TTT CAT GGC TGT TAT TTT ATG GGA
Leu Ile Arg Ala Ser Thr His Val Leu Phe His Gly Cys Tyr Phe Met Gly

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FIG. 1G

2430	2440	2450	2460	2470
ATT ATG GGC ACT TGT ATT GAG GTG GCG GGA GCT TAC ATT CGG GGT TGT				
Ile Met Gly Thr Cys Ile Glu Val Gly Ala Gly Ala Tyr Ile Arg Gly Cys				
2480	2490	2500	2510	2520
GAG TTT GTG GGC TGT TAC CGG GGA ATC TGT TCT ACT TCT AAC AGA GAT ATT				
Glu Phe Val Gly Cys Tyr Arg Gly Ile Cys Ser Thr Ser Asn Arg Asp Ile				
2530	2540	2550	2560	2570
AAG GTG AGG CAG TGC AAC TTT GAC AAA TGC TTA CTG GGT ATT ACT TGT AAG				
Lys Val Arg Gln Cys Asn Phe Asp Lys Cys Leu Leu Gly Ile Thr Cys Lys				
2580	2590	2600	2610	2620
GGG GAC TAT CGT CTT TCG GGA AAT GTG TGT TCT GAG ACT TTC TGC TTT GCT				
Gly Asp Tyr Arg Leu Ser Gly Asn Val Cys Ser Glu Thr Phe Cys Phe Ala				
2630	2640	2650	2660	2670
CAT TTA GAG GGA GGT TTG GTT AAA AAC AAC ACA GTC AAG TCC CCT AGT				
His Leu Glu Gly Glu Gly Leu Val Lys Asn Asn Thr Val Lys Ser Pro Ser				
2680	2690	2700	2710	2720
CGC TGG ACC AGC GAG TCT GGC TTT TCC ATG ATA ACT TGT GCA GAC GGC AGG				
Arg Trp Thr Ser Glu Ser Gly Phe Ser Met Ile Thr Cys Ala Asp Gly Arg				

FIG. 1H


```
2730      2740      2750      2760      2770
GTT ACG CCT TTG GGT TCC CTC CAC ATT GTG GGC AAC CGT TGT AGG CGT TGG
Val Thr Pro Leu Gly Ser Leu His Ile Val Gly Asn Arg Cys Arg Arg Trp

2780      2790      2800      2810      2820      2830
CCA ACC ATG CAG GGG AAT GTG TTT ATC ATG TCT AAA CTG TAT CTG GGC AAC
Pro Thr Met Gln Gly Asn Val Phe Ile Met Ser Lys Leu Tyr Leu Gly Asn

2840      2850      2860      2870      2880
AGA ATA GGG ACT GTA GCC CTG CCC CAG TGT GCT TTC TAC AAG TCC AGC ATT
Arg Ile Gly Thr Val Ala Leu Pro Gln Cys Ala Phe Tyr Lys Ser Ser Ile

2890      2900      2910      2920      2930
TGT TTG GAG GAG AGG GCG ACA AAC AAG CTG GTC TTG GCT TGT GCT TTT GAG
Cys Leu Glu Glu Arg Ala Thr Asn Lys Leu Val Leu Ala Cys Ala Phe Glu

2940      2950      2960      2970      2980
AAT AAT GTA CTG GTG TAC AAA GTG CTG AGA CCG GAG AGT CCC TCA ACC GTG
Asn Asn Val Leu Val Tyr Lys Val Leu Arg Arg Glu Ser Pro Ser Thr Val

2990      3000      3010      3020      3030
AAA ATG TGT GTT TGT GGG ACT TCT CAT TAT GCA AAG CCT TTG ACA CTG GCA
Lys Met Cys Val Cys Gly Thr Ser His Tyr Ala Lys Pro Leu Thr Leu Ala
```

FIG. 11

```
3040      3050      3060      3070      3080
ATT ATT TCT TCA GAT ATT CGG GCT AAT CGA TAC ATG TAC ACT GTG GAC TCA
Ile Ile Ser Ser Asp Ile Arg Ala Asn Arg Tyr Met Tyr Thr Val Asp Ser

3090      3100      3110      3120      3130      3140
ACA GAG TTC ACT TCT GAC GAG GAT T AAAAGTGGC GGGGCCAAGA GGGGTATAAA
Thr Glu Phe Thr Ser Asp Glu Asp End

3150      3160      3170      3180      3190      3200
TAGTGGGGA GGTGAGGG AGCCGTAGTT TCTGTTTTC CCAGACTGGG GGGGACAAC ATG
Met

3210      3220      3230      3240      3250
GCC GAG GAA GGG CGC ATT TAT GTG CCT TAT GTA ACT GCC CGC CTG CCC AAG
Ala Glu Glu Gly Arg Ile Tyr Val Pro Tyr Val Thr Ala Arg Leu Pro Lys

3260      3270      3280      3290      3300
TGG TCG GGT TCG GTG CAG GAT AAG ACG GGC TCG AAC ATG TTG GGG GGT GTG
Trp Ser Gly Ser Val Gln Asp Lys Thr Gly Ser Asn Met Leu Gly Gly Val

3310      3320      3330      3340      3350
GTA CTC CCT CCT AAT TCA CAG GCG CAC CGG ACG GAG ACC GTG GGC ACT GAG
Val Leu Pro Pro Asn Ser Gln Ala His Arg Thr Glu Thr Val Gly Thr Glu
```

FIG. 1J

```
3360      3370      3380      3390      3400
GCC ACC AGA GAC AAC CTG CAC GCC GAG GGA GCG CGT CGT CCT GAG GAT CAG
Ala Thr Arg Asp Asn Leu His Ala Glu Gly Ala Arg Arg Pro Glu Asp Gln

3410      3420      3430      3440      3450
ACG CCC TAC ATG ATC TTG GTG GAG GAC TCT CTG GGA GGT TTG AAG AGG CGA
Thr Pro Tyr Met Ile Leu Val Glu Asp Ser Leu Gly Gly Leu Lys Arg Arg

3460      3470      3480      3490      3500
ATG GAC TTG CTG GAA GAA TCT AAT CAG CAG CTG CTG GCA ACT CTC AAC CGT
Met Asp Leu Leu Glu Glu Ser Asn Gln Gln Leu Leu Ala Thr Leu Asn Arg

3510      3520      3530      3540      3550
CTC CGT ACA GGA CTC GCT GCC TAT GTG CAG GCT AAC CTT GTG GGC GGC CAA
Leu Arg Thr Gly Leu Ala Ala Tyr Val Gln Ala Asn Leu Val Gly Gly Gln

3560      3570      3580      3590      3600      3610
GTT AAC CCC TTT GTT TAAATA AAAATACACT CATACAGTTT ATTATGCTGT
Val Asn Pro Phe Val End

3620      3630      3640      3650      3660      3670
CAATAAAATT CTTTATTTT CCTGTGATAA TACCGTGTCC AGCGTGCTCT GTCAATAAGG

3680      3690      3700      3710      3720      3730
GTCCTATGCA TCCTGAGAAG GGCCTCATAT ACCCATGGCA TGAATATTAA GATACATGGG
```

FIG. 1K

3740 3750 3760 3770 3780 3790
CATAAGGCC TCAGAAGGT TGAGGTAGAG CCACTGCAGA CTTTCGTGG GAGTAAGGT
3800 3810 3820 3830 3840 3850
GTTGTAATA ATCCAGTCAT ACTGACTGTG CTGGCGGTGG AAGGAAAAGA TGTCTTTAG
3860 3870 3880 3890 3900 3910
AAGAAGGTG ATTGGCAAAG GGAGGCTCTT AGTGTAGGTA TTGATAAATC TGTTCAGTTG
3920 3930 3940 3950 3960 3970
GGAGGGATGC ATTGGGGGC TAATAAGGTG GAGTTTAGCC TGAATCTTAA GGTTGGCAAT
3980 3990 4000 4010 4020 4030
GTTGCCCCCT AGGTCTTTGC GAGGATTTCAT GTTGTGCAGT ACCACAAAAA CAGAGTAGCC
4040 4050 4060
TGTGCATTG GGGAATTTAT CATGAAGCT T

FIG. 1L

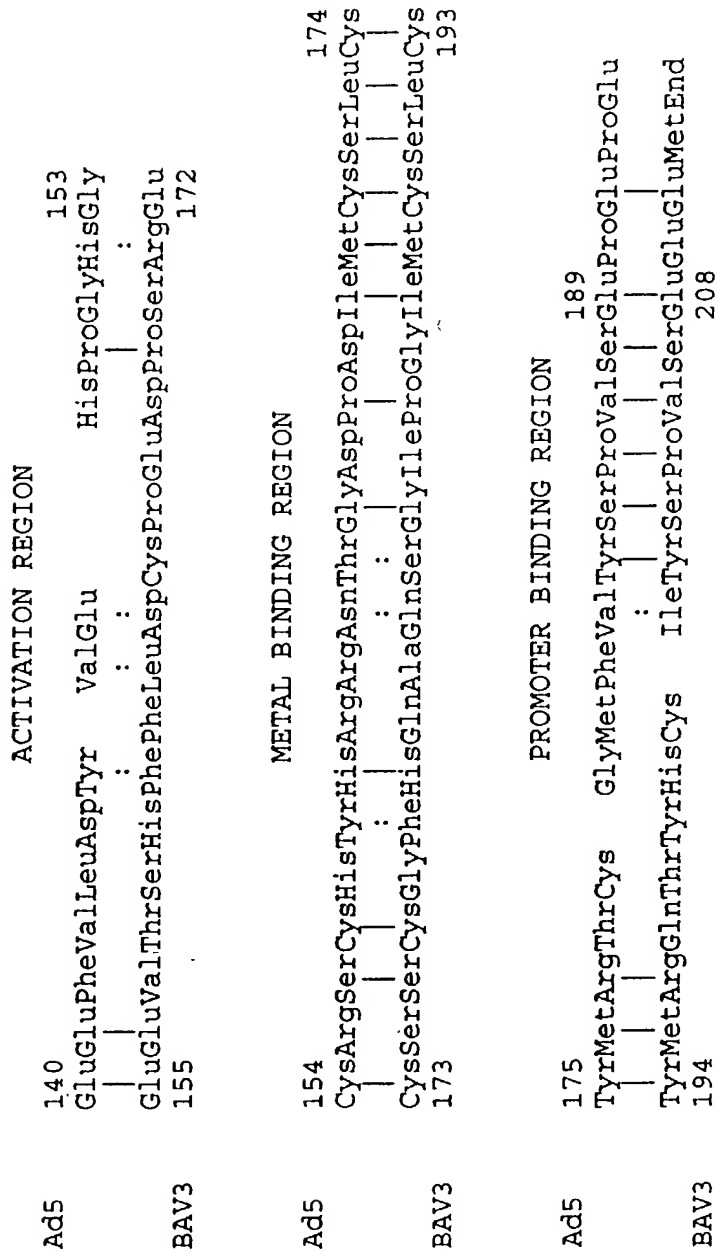


FIG. 2A

Rb BINDING SEQUENCE

Ad5	120	IleAspLeuThrCysHisGluAlaGlyPheProProSer	132
		:	
		ValAspLeuGluCysHisGluVal	LeuProProSer
BAV3	26		37

FIG. 2B

Ad5	82	LeuAspPheSerThrProGlyArgAlaAlaAlaAlaValAlaPheLeuSerPheIle	100
		LeuAsp	ThrProGlyArgValValAlaAlaLeuAlaLeuLeuValPheIle
BAV3	83		99

FIG. 3A

Ad5	20	GlnSerSerAsnSerThrSer	26
		GlnSerSerArgSerThrSer	
BAV3	136		142

FIG. 3B

Ad5 150 GlnLysTyrSerIleGluGlnLeuThrThrTyrTrpLeuGlnProGlyAspAspPheGlu
 : | | | : : | | |
 BAV3 74 GluArgTyrSerPheGluAspIleLysSerTyrGluAlaLeuProGluAspAsnLeuGlu
 170 GluAlaIleArgValTyrAlaLysValAlaLeuArgProAspCysLysTyrLysIleSer
 | : | | : | | | : :
 94 GlnLeuIleAlaMetHisAlaLysIleLysLeuLeuProGlyArgGluTyrGluLeuThr
 190 LysLeuValAsnIleArgAsnCysCysTyrIleSerGlyAsnGlyAlaGluValGluIle
 : | | | : | | | | : :
 114 GlnProLeuAsnIleThrSerCysAlaTyrValLeuGlyAsnGlyAlaThrIleArgVal
 210 AspThrGluAspArgValAlaPheArgCysSerMetIleAsnMetTrpProGlyValLeu
 | | | : : | | |
 134 ThrGlyGluAlaSerProAlaIleArgValGlyAlaMetAlaValGlyProCysValThr
 230 GlyMetAspGlyValValIleMetAsnValArgPheThr GlyProAsnPheSerGly
 | | | : | | | |
 154 GlyMetThrGlyValThrPheValAsnCysArgPheGluArgGluSerThrIleArgGly
 249 ThrValPheLeuAlaAsnThrAsnLeuIleLeuHisGlyValSerPheTyr GlyPhe
 : : | | : : | | : : |
 174 SerLeuIleArgAlaSerThrHisValLeuPheHisGlyCys TyrPheMetGlyIle
 268 AsnAsnThrCysValGluAlaTrpThrAspValArgValArgGlyCysAlaPheTyrCys
 | | : |
 193 MetGlyThrCysIleGluValGlyAlaGlyAlaTyrIleArgGlyCysGluPheValGly
 288 CysTrpLysGlyValValCysArgProLysSerArgAla SerIleLysLysCysLeu
 | : : | : | : : |
 213 CysTyrArgGlyIle CysSerThrSerAsnArgAspIleLysValArgGlnCysAsn
 307 PheGluArgCysThrLeuGlyIleLeuSerGluGlyAsnSerArgValArgHisAsnVal
 | : : | | | | | : | |
 232 PheAspLysCysLeuLeuGlyIleThrCysLysGlyAspTyrArgLeuSerGlyAsnVal
 327 AlaSerAspCysGlyCysPheMetLeuValLysSerValAlaValIleLysHisAsnMet
 | : | | : : | |
 252 CysSerGluThrPheCysPheAlaHisLeuGluGlyGluGlyLeuValLysAsnAsnThr

FIG. 4A

347 Val CysGlyAsn CysGluAspArgAlaSerGlnMetLeuThrCysSerAsp
 | : | | : |
 272 ValLysSerProSerArgTrpThrSerGluSerGlyPheSerMetIleThrCysAlaAsp
 364 GlyAsnCysHisLeuLeuLysThrIleHisVal AlaSerHisSerArgLysAlaTrp
 | : : | : : | : |
 292 GlyArgValThrProLeuGlySerLeuHisIleValGlyAsnArgCysArgArg Trp
 383 ProValPheGluHisAsnIleLeuHisArgCysSerLeuHisLeuGlyAsnArgArgGly
 | : | | | | | |
 311 ProThrMetGlnGlyAsnValPheIleMetSerLysLeuTyrLeuGlyAsnArgIleGly
 403 ValPheLeuProTyrGlnCysAsnLeuSerHisThrLysIleLeuLeuGluProGlu
 | | | | : : | | |
 331 ThrValAlaLeuPro GlnCysAlaPheTyrLysSerSerIleCysLeuGluGluArg
 422 SerMetSerLysValAsnLeuAsnGlyValPheAspMetThrMetLysIleTrpLysVal
 : | : | : : : : | |
 350 AlaThrAsnLysLeuValLeuAlaCysAlaPheGluAsnAsnValLeuValTyrLysVal
 442 LeuArgTyrAspGluThrArgThrArgCysArgProCysGluCysGlyGlyLysHisIle
 | | : | : | | | |
 370 LeuArgArgGluSerProSerThr ValLysMetCysValCysGlyThrSerHisTyr
 462 ArgAsnGlnProValMetLeuAspVal ThrGluGluLeuArgProAspHisLeuVal
 | : | : : : | : :
 389 AlaLysProLeuThrLeuAlaIleIleSerSerAspIleArgAlaAsnArgTyrMet
 481 LeuAlaCysHisArgAlaGluPheGlySerSerAspGluAspThrAspEnd
 : : | | : | | | |
 408 TyrThrValAspSerThrGluPhe ThrSerAspGluAspEnd

FIG. 4B


```

Ad5      1  MetSerThrAsnSerPheAspGlySerIleValSerSerTyrLeuThrThrArgMetPro
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
BAV3     1  MetAla  Glu  GluGlyArgIleTyrValProTyrValThrAlaArgLeuPro
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          21  ProTrpAlaGlyValArgGlnAsnValMetMetGlySerSerIleAspGlyArgProValLeu
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          18  LysTrpSerGlySerValGlnAspLysThrGlySerAsnMetLeuGlyGlyValValLeu
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          41  ProAlaAsnSerThrThrLeuThrTyrGluThrValSerGlyThrProLeuGluThrAla
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          38  ProProAsnSerGlnAlaHisArgThrGluThrVal  GlyThrGlu  AlaThr
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          61  AlaSerAlaAlaAlaSerAlaAlaAlaAlaThrAlaArgGlyIleValThrAspPheAla
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          55  ArgAspAsnLeuHisAlaGluGlyAlaArg  ArgProGluAspGlnThr  Pro
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          81  PheLeuSerProLeuAlaSerSerAlaAlaAlaSerArgSerSerAlaArgAspLysLeu
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          72  TyrMetIle  LeuValGluAspSerLeuGlyGlyLeuLysArgArgMetAspLeuLeu
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          101  ThrAlaLeuLeuAlaGlnLeu  AspSerLeuThrArgGluLeuAsnValValSerGln
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          91  GluGluSerAsnGlnGlnLeuLeuAlaThrLeuAsnArg  LeuArgThr  Gly
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          120  GlnLeuLeuAspLeuArgGlnGlnValSerAlaLeuLysAlaSerSerProProAsnAla
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          108  LeuAlaAlaTyr  valGln  AlaAsnLeuValGlyGlyGlnValAsnProphe
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          140  ValEnd
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
          125  ValEnd
  
```

FIG. 5

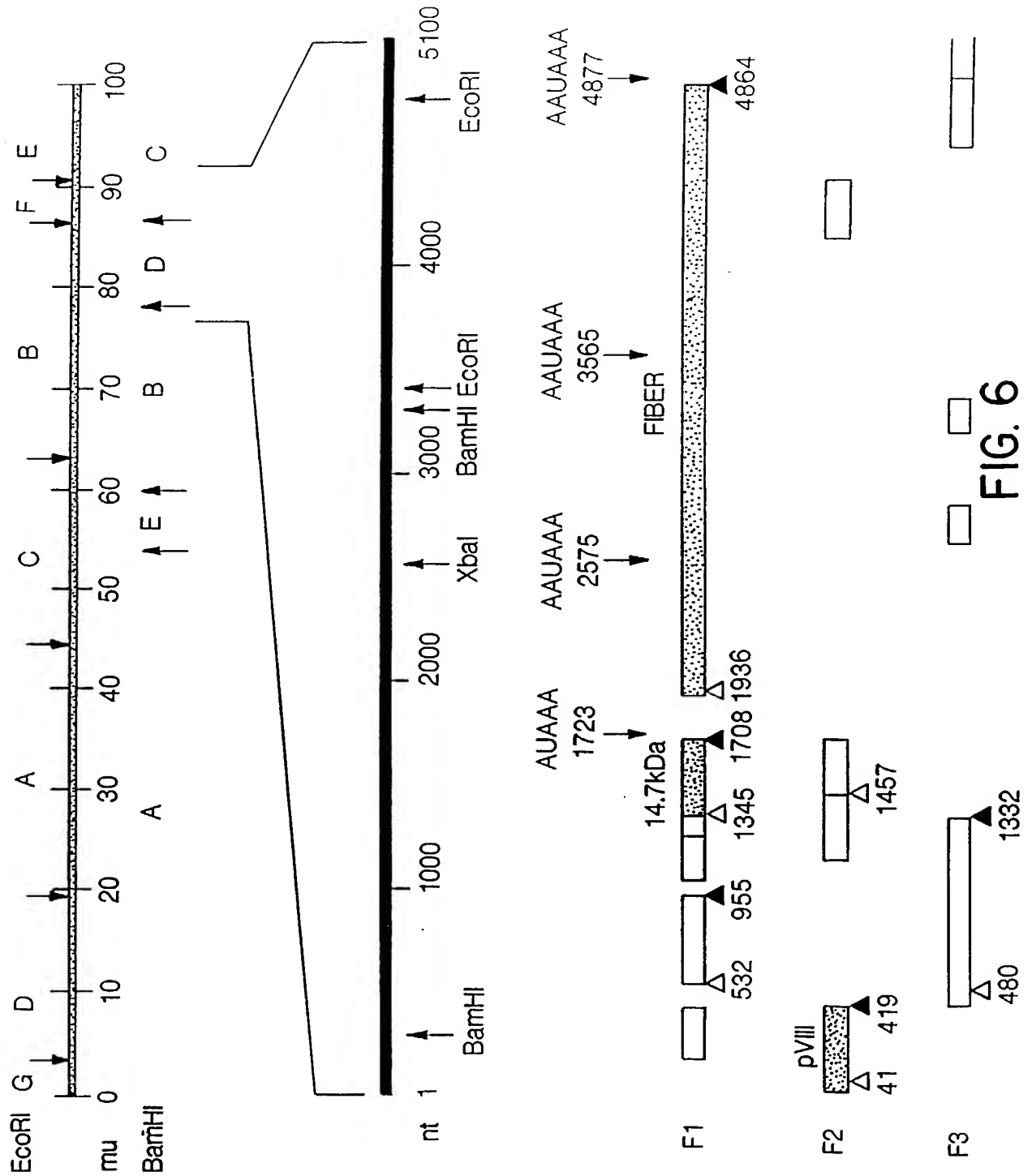


FIG. 6

ORF 1 C CTC ATC AAA CAA CCC GTG GTG ACC ACC CAC GTG GAA ATG CCT CGC AAC
10 20 30 40 50
Leu Ile Lys Gln Pro Val Val Gly Thr Thr His Val Glu Met Pro Arg Asn
60 70 80 90 100
GAA GTC CTA GAA CAA CAT CTG ACC TCA CAT GGC GCT CAA ATC GCG GGC GGA
Glu Val Leu Glu Gln His Leu Thr Ser His Gly Ala Gln Ile Ala Gly Gly
110 120 130 140 150
GGC GCT GCG GGC GAT TAC TTT AAA AGC CCC ACT TCA GCT CGA ACC CTT ATC
Gly Ala Ala Gly Asp Tyr Phe Lys Ser Pro Thr Ser Ala Arg Thr Leu Ile
160 170 180 190 200
CCG CTC ACC GCC TCC TGC TTA AGA CCA GAT GGA GTC TTT CAA CTA GGA GGA
Pro Leu Thr Ala Ser Cys Leu Arg Pro Asp Gly Val Phe Gln Leu Gly Gly
210 220 230 240 250
GGC TCG CGT TCA TCT TTC AAC CCC CTG CAA ACA GAT TTT GCC TTC CAC GCC
Gly Ser Arg Ser Ser Phe Asn Pro Leu Gln Thr Asp Phe Ala Phe His Ala
260 270 280 290 300
CTG CCC TCC AGA CCG CGC CAC GGG GGC ATA GGA TCC AGG CAG TTT GTA GAG
Leu Pro Ser Arg Pro Arg His Gly Gly Ile Gly Ser Arg Gln Phe Val Glu

FIG. 7A

310 320 330 340 350
GAA TTT GTG CCC GCC GTC TAC CTC AAC CCC TAC TCG GGA CCG CCG GAC TCT
Glu Phe Val Pro Ala Val Tyr Leu Asn Pro Tyr Ser Gly Pro Pro Asp Ser

360 370 380 390 400
TAT CCG GAC CAG TTT ATA CGC CAC TAC AAC GTG TAC AGC AAC TCT GTG AGC
Tyr Pro Asp Gln Phe Ile Arg His Tyr Asn Val Tyr Ser Asn Ser Val Ser
ORF 2 Ala

410 420 430 440 450 460
GGT TAT AGC T GAG ATT GTA AGA CTC TCC TAT CTG TCT CTG TGC TGC TTT TCC
Gly Tyr Ser
Val Ile Ala Glu Ile Val Arg Leu Ser Tyr Leu Ser Leu Cys Phe Ser

470 480 490 500 510
GCT TCA AGC CCC ACA AGC ATG AAG GGG TTT CTG CTC ATC TTC AGC CTG CTT
Ala Ser Ser Pro Thr Ser Met Lys Gly Phe Leu Leu Ile Phe Ser Leu Leu

520 530 540 550 560
GTG CAT TGT CCC CTA ATT CAT GTT GGG ACC ATT AGC TTC TAT GCT GCA AGG
ORF 3 Phe Met Leu Gly Pro Leu Ala Ser Met Leu Gln Gly
Val His Cys Pro Leu Ile His Val Gly Thr Ile Ser Phe Tyr Ala Ala Arg

FIG. 7B

570 580 590 600 610
CCC GGG TCT GAG CCT AAC GCG ACT TAT GTT TGT GAC TAT GGA AGC GAG TCA
Pro Gly Leu Ser Leu Thr Arg Leu Met Phe Val Thr Met Glu Ala Ser Gln
Pro Gly Ser Glu Pro Asn Ala Thr Tyr Val Cys Asp Tyr Gly Ser Glu Ser

620 630 640 650 660
GAT TAC AAC CCC ACC ACG GTT CTG TGG TTG GCT CGA GAG ACC GAT GGC TCC
Ile Thr Thr Pro Pro Arg Phe Cys Gly Trp Leu Glu Arg Pro Met Ala Pro
Asp Tyr Asn Pro Thr Val Leu Trp Leu Ala Arg Glu Thr Asp Gly Ser

670 680 690 700 710
TGG ATC TCT GTT CTT TTC CGT CAC AAC GGC TCC TCA ACT GCA GCC CCC GGG
Gly Ser Leu Phe Phe Ser Val Thr Thr Ala Pro Gln Leu Gln Pro Pro Gly
Trp Ile Ser Val Leu Phe Arg His Asn Gly Ser Ser Thr Ala Ala Pro Gly

720 730 740 750 760
GTC GTC GCG CAC TTT ACT GAC CAC AAC AGC AGC ATT GTG GTG CCC CAG TAT
Ser Ser Arg Thr Leu Leu Thr Thr Thr Ala Ala Leu Trp Cys Pro Ser Ile
Val Val Ala His Phe Thr Asp His Asn Ser Ser Ile Val Val Pro Gln Tyr

770 780 790 800 810
TAC CTC CTC AAC AAC TCA CTC TCT AAG CTC TGC TGC TCA TAC CGG CAC AAC
Thr Ser Ser Thr Thr His Ser Leu Ser Ser Ala Ala His Thr Gly Thr Thr
Tyr Leu Leu Asn Asn Ser Leu Ser Lys Ser Cys Ser Tyr Arg His Asn

FIG. 7C

820 830 840 850 860
GAG CGT TCT CAG TTT ACC TGC AAA CAA GCT GAC GTC CCT ACC TGT CAC GAG
Ser Val Leu Ser Leu Pro Ala Asn Lys Leu Thr Ser Leu Pro Val Thr Ser
Glu Arg Ser Gln Phe Thr Cys Lys Gln Ala Asp Val Pro Thr Cys His Glu

870 880 890 900 910 920
CCC GGC AAG CCG CTC ACC CTC CGC GTC TCC CCC GCG CTG GGA ACT GCC CAC
Pro Ala Ser Arg Ser Pro Ser Ala Ser Pro Pro Arg Trp Glu Leu Pro Thr
Pro Gly Lys Pro Leu Thr Leu Arg Val Ser Pro Ala Leu Gly Thr Ala His

930 940 950 960 970
CAA GCA GTC ACT TGG TTT TTT CAA AAT GTA CCC ATA GCT ACT GTT TAC CGA
Lys Gln Ser Leu Gly Phe Phe Lys Met Tyr Pro
Gln Ala Val Thr Trp Phe Phe Gln Asn Val Pro Ile Ala Thr Val Tyr Arg

980 990 1000 1010 1020
CCT TGG GGC AAT GTA ACT TGG TTT TGT CCT CCC TTC ATG TGT ACC TTT AAT
Pro Trp Gly Asn Val Thr Trp Phe Cys Pro Pro Phe Met Cys Thr Phe Asn

1030 1040 1050 1060 1070
GTC AGC CTG AAC TCC CTA CTT ATT TAC AAC TTT TCT GAC AAA ACC GGG GGG
Val Ser Leu Asn Ser Leu Leu Ile Tyr Asn Phe Ser Asp Lys Thr Gly Gly

FIG. 7D

```
1080      1090      1100      1110      1120
CAA TAC ACA GCT CTC ATG CAC TCC GGA CCT GCT TCC CTC TTT CAG CTC TTT
Gln Tyr Thr Ala Leu Met His Ser Gly Pro Ala Ser Leu Phe Gln Leu Phe

1130      1140      1150      1160      1170
AAG CCA ACG ACT TGT GTC ACC AAG GTG GAG GAC CCG CCG TAT GCC AAC GAC
Lys Pro Thr Thr Cys Val Thr Lys Val Glu Asp Pro Pro Tyr Ala Asn Asp

1180      1190      1200      1210      1220
CCG GCC TCG CCT GTG TGG CGC CCA CTG CTT TTT GCC TTC GTC CTC TGC ACC
Pro Ala Ser Pro Val Trp Arg Pro Leu Leu Phe Ala Phe Val Leu Cys Thr

1230      1240      1250      1260      1270
GGC TGC GCG GTG TTG TTA ACC GCC TTC GGT CCA TCG ATT CTA TCC GGT ACC
ORF 4 Pro Pro Ser Val His Arg Phe Tyr Pro Val Pro
Gly Cys Ala Val Leu Leu Thr Ala Phe Gly Pro Ser Ile Leu Ser Gly Thr

1280      1290      1300      1310      1320
CGA AAG CTT ATC TCA GCC CGC TTT TGG AGT CCC GAG CCC TAT ACC ACC CTC
Glu Ser Leu Ser Gln Pro Ala Phe Gly Val Pro Ser Pro Ile Pro Pro Ser
Arg Lys Leu Ile Ser Ala Arg Phe Trp Ser Pro Glu Pro Tyr Thr Thr Leu
```

FIG. 7E

1330 1340 1350 1360 1370 1380
 CAC T AAC AGT CCC CCC ATG GAG CCA GAC GGA GTT CAT GCC GAG CAG CAG TTT
 Thr Asn Ser Pro Pro Met Glu Pro Asp Gly Val His Ala Glu Gln Gln Phe
 His

1390 1400 1410 1420 1430
 ATC CTC AAT CAG ATT TCC TGC GCC AAC ACT GCC CTC CAG CGT CAA AGG GAG
 Ile Leu Asn Gln Ile Ser Cys Ala Asn Thr Ala Leu Gln Arg Gln Arg Glu

1440 1450 1460 1470 1480
 GAA CTA GCT TCC CTT GTC ATG TTG CAT GCC TGT AAG CGT GGC CTC TTT TGT
 Glu Leu Ala Ser Leu Val Met Leu His Ala Cys Lys Arg Gly Leu Phe Cys
 ORF 5 Leu Pro Leu Ser Cys Cys Met Pro Val Ser Val Ala Ser Phe Val

1490 1500 1510 1520 1530
 CCA GTC AAA ACT TAC AAG CTC AGC CTC AAC GCC TCG GCC AGC GAG CAC AGC
 Pro Val Lys Thr Tyr Lys Leu Ser Leu Asn Ala Ser Ala Ser Glu His Ser
 Gln Ser Lys Leu Thr Ser Ser Ala Ser Thr Pro Arg Pro Ala Ser Thr Ala

1540 1550 1560 1570 1580
 CTG CAC TTT GAA AAA AGT CCC TCC CGA TTC ACC CTG GTC AAC ACT CAC GCC
 Leu His Phe Glu Lys Ser Pro Ser Arg Phe Thr Leu Val Asn Thr His Ala
 Cys Thr Leu Lys Lys Val Pro Pro Asp Ser Pro Trp Ser Thr Leu Thr Pro

FIG. 7F


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1590      1600      1610      1620      1630
GGA GCT TCT GTG CGA GTG GCC CTA CAC CAC CAG GGA GCT TCC GGC AGC ATC
Gly Ala Ser Val Arg Val Ala Leu His His Gln Gly Ala Ser Gly Ser Ile
Glu Leu Leu Cys Glu Trp Pro Tyr Thr Thr Arg Glu Leu Pro Ala Ala Ser

1640      1650      1660      1670      1680
CGC TGT TCC TGT TCC CAC GCC GAG TGC CTC CCC GTC CTC CTC AAG ACC CTC
Arg Cys Ser Cys Ser His Ala Glu Cys Leu Pro Val Leu Leu Lys Thr Leu
Ala Val Pro Val Pro Thr Pro Ser Ala Ser Pro Ser Ser Ser Arg Pro Ser

1690      1700      1710      1720      1730      1740
TGT GCC TTT AAC TTT TTA GAT TAG CTGAAAGCAA ATATAAAATG GTGTGCTTAC
Cys Ala Phe Asn Phe Leu Asp
Val Pro Leu Thr Phe

1750      1760      1770      1780      1790
CGTAATCTG TTTTGACTTG TGTGCTTGA TTT CTC CCC CTG CGC CGT AAT CCA GTG

1800      1810      1820      1830      1840
CCC CTC TTC AAA ACT CTC GTA CCC TAT GCG ATT CGC ATA GGC ATA TTT TCT

1850      1860      1870      1880      1890
AAA AGC TCT GAA GTC AAC ATC ACT CTC AAA CAC TTC TCC GTT GTA GGT TAC
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FIG. 7G

1900 1910 1920 1930 1940 1950
 TTT CAT CTA CAG ATA AAG TCA TCC ACC GGT T AAC ATC ATG AAG AGA AGT GTG
 ORF 6 Ser His Pro Pro Val Asn Ile Met Lys Arg Ser Val

1960 1970 1980 1990 2000
 CCC CAG GAC TTT AAT CTT GTG TAT CCG TAC AAG GCT AAG AGG CCC AAC ATC
 Pro Gln Asp Phe Asn Leu Val Tyr Pro Tyr Lys Ala Lys Arg Pro Asn Ile

2010 2020 2030 2040 2050
 ATG CCG CCC TTT TTT GAC CGC AAT GGC TTT GTT GAA AAC CAA GAA GCC ACG
 Met Pro Pro Phe Phe Asp Arg Asn Gly Phe Val Glu Asn Gln Glu Ala Thr

2060 2070 2080 2090 2100
 CTA GCC ATG CTT GTG GAA AAG CCG CTC ACG TTC GAC AAG GAA GGT GCG CTG
 Leu Ala Met Leu Val Glu Lys Pro Leu Thr Phe Asp Lys Glu Gly Ala Leu

2110 2120 2130 2140 2150
 ACC CTG GGC GTC GGA CGC GGC ATC CGC ATT AAC CCC GCG GGG CTT CTG GAG
 Thr Leu Gly Val Gly Arg Gly Ile Arg Ile Asn Pro Ala Gly Leu Leu Glu

2160 2170 2180 2190 2200
 ACA AAC GAC CTC GCG TCC GCT GTC TTC CCA CCG CTG GCC TCC GAT GAG GCC
 Thr Asn Asp Leu Ala Ser Ala Val Phe Pro Pro Leu Ala Ser Asp Glu Ala

FIG. 7H

2210 2220 2230 2240 2250
GGC AAC GTC ACG CTC AAC ATG TCT GAC GGG CTA TAT ACT AAG GAC AAC AAG
Gly Asn Val Thr Leu Asn Met Ser Asp Gly Leu Tyr Thr Lys Asp Asn Lys

2260 2270 2280 2290 2300
CTA GCT GTC AAA GTA GGT CCC GGG CTG TCC CTC GAC TCC AAT AAT GCT CTC
Leu Ala Val Lys Val Gly Pro Gly Leu Ser Leu Asp Ser Asn Asn Ala Leu

2310 2320 2330 2340 2350
CAG GTC CAC ACA GGC GAC GGG CTC ACG GTA ACC GAT GAC AAG GTG TCT CTA
Gln Val His Thr Gly Asp Gly Leu Thr Val Thr Asp Asp Lys Val Ser Leu

2360 2370 2380 2390 2400
AAT ACC CAA GCT CCC CTC TCG ACC ACC ACG GCG GGC CTC TCC CTA CTT CTG
Asn Thr Gln Ala Pro Leu Ser Thr Thr Ser Ala Gly Leu Ser Leu Leu Leu

2410 2420 2430 2440 2450 2460
GGT CCC AGC CTC CAC TTA GGT GAG GAG GAA CGA CTA ACA GTA AAC ACC GGA
Gly Pro Ser Leu His Leu Gly Glu Glu Arg Leu Thr Val Asn Thr Gly

2470 2480 2490 2500 2510
GCG GGC CTC CAA ATT AGC AAT AAC GCT CTG GCC GTA AAA GTA GGT TCA GGT
Ala Gly Leu Gln Ile Ser Asn Asn Ala Leu Ala Val Lys Val Gly Ser Gly

FIG. 7I

2520 2530 2540 2550 2560
ATC ACC GTA GAT GCT CAA AAC CAG CTC GCT GCA TCC CTG GGG GAC GGT CTA
Ile Thr Val Asp Ala Gln Asn Gln Leu Ala Ala Ser Leu Gly Asp Gly Leu

2570 2580 2590 2600 2610
GAA AGC AGA GAT AAT AAA ACT GTC GTT AAG GCT GGG CCC GGA CTT ACA ATA
Glu Ser Arg Asp Asn Lys Thr Val Val Lys Ala Gly Pro Gly Leu Thr Ile

2620 2630 2640 2650 2660
ACT AAT CAA GCT CTT ACT GTT GCT ACC GGG AAC GGC CTT CAG GTC AAC CCG
Thr Asn Gln Ala Leu Thr Val Ala Thr Gly Asn Gly Leu Gln Val Asn Pro

2670 2680 2690 2700 2710
GAA GGG CAA CTG CAG CTA AAC ATT ACT GCC GGT CAG GGC CTC AAC TTT GCA
Glu Gly Gln Leu Gln Leu Asn Ile Thr Ala Gly Gln Gly Leu Asn Phe Ala

2720 2730 2740 2750 2760
AAC AAC AGC CTC GCC GTG GAG CTG GGC TCG GGC CTG CAT TTT CCC CCT GGC
Asn Asn Ser Leu Ala Val Glu Leu Gly Ser Gly Leu His Phe Pro Pro Gly

2770 2780 2790 2800 2810
CAA AAC CAA GTA AGC CTT TAT CCC GGA GAT GGA ATA GAC ATC CGA GAT AAT
Gln Asn Gln Val Ser Leu Tyr Pro Gly Asp Gly Ile Asp Ile Arg Asp Asn

FIG. 7J

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2820      2830      2840      2850      2860
AGG GTG ACT GTG CCC GCT GGG CCA GGC CTG AGA ATG CTC AAC CAC CAA CTT
Arg Val Thr Val Pro Ala Gly Pro Gly Leu Arg Met Leu Asn His Gln Leu

2870      2880      2890      2900      2910
GCC GTA GCT TCC GGA GAC GGT TTA GAA GTC CAC AGC GAC ACC CTC CGG TTA
Ala Val Ala Ser Gly Asp Gly Leu Glu Val His Ser Asp Thr Leu Arg Leu

2920      2930      2940      2950      2960      2970
AAG CTC TCC CAC GGC CTG ACA TTT GAA AAT GGC GCC GTA CGA GCA AAA CTA
Lys Leu Ser His Gly Leu Thr Phe Glu Asn Gly Ala Val Arg Ala Lys Leu

2980      2990      3000      3010      3020
GGA CCA GGA CTT GGC ACA GAC GAC TCT GGT CGG TCC GTG GTT CGC ACA GGT
Gly Pro Gly Leu Gly Thr Asp Asp Ser Gly Arg Ser Val Val Arg Thr Gly

3030      3040      3050      3060      3070
CGA GGA CTT AGA GTT GCA AAC GGC CAA GTC CAG ATC TTC AGC GGA AGA GGC
Arg Gly Leu Arg Arg Val Ala Asn Gly Gln Val Gln Ile Phe Ser Gly Arg Gly

3080      3090      3100      3110      3120
ACC GCC ATC GGC ACT GAT AGC AGC CTC ACT CTC AAC ATC CGG GCG CCC CTA
Thr Ala Ile Gly Thr Asp Ser Ser Leu Thr Leu Asn Ile Arg Ala Pro Leu

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FIG. 7K

3130 3140 3150 3160 3170
CAA TTT TCT GGA CCC GCT TTG ACT GCT AGT TTG CAA GGC AGT GGT CCG ATT
Gln Phe Ser Gly Pro Ala Leu Thr Ala Ser Leu Gln Gly Ser Gly Pro Ile

3180 3190 3200 3210 3220
ACT TAC AAC AGC AAC AAT GGC ACT TTC GGT CTC TCT ATA GGC CCC GGA ATG
Thr Tyr Asn Ser Asn Asn Gly Thr Phe Gly Leu Ser Ile Gly Pro Gly Met

3230 3240 3250 3260 3270
TGG GTA GAC CAA AAC AGA CTT CAG GTA AAC CCA GGC GCT GGT TTA GTC TTC
Trp Val Asp Gln Asn Arg Leu Gln Val Asn Pro Gly Ala Gly Leu Val Phe

3280 3290 3300 3310 3320
CAA GGA AAC AAC CTT GTC CCA AAC CTT GCG GAT CCG CTG GCT ATT TCC GAC
Gln Gly Asn Asn Leu Val Pro Asn Leu Ala Asp Pro Leu Ala Ile Ser Asp

3330 3340 3350 3360 3370
AGC AAA ATT AGT CTC AGT CTC GGT CCC GGC CTG ACC CAA GCT TCC AAC GCC
Ser Lys Ile Ser Leu Ser Leu Gly Pro Gly Leu Thr Gln Ala Ser Asn Ala

3380 3390 3400 3410 3420
CTG ACT TTA AGT TTA GGA AAC GGG CTT GAA TTC TCC AAT CAA GCC GTT GCT
Leu Thr Leu Ser Leu Gly Asn Gly Leu Glu Phe Ser Asn Gln Ala Val Ala

FIG. 7L

3430 3440 3450 3460 3470 3480
 ATA AAA GCG GGC CGG GGC TTA CGC TTT GAG TCT TCC TCA CAA GCT TTA GAG
 Ile Lys Ala Gly Arg Gly Leu Arg Phe Glu Ser Ser Ser Gln Ala Leu Glu

3490 3500 3510 3520 3530
 AGC AGC CTC ACA GTC GGA AAT GGC TTA ACG CTT ACC GAT ACT GTG ATC CGC
 Ser Ser Leu Thr Val Gly Asn Gly Leu Thr Leu Thr Asp Thr Val Ile Arg

3540 3550 3560 3570 3580
 CCC AAC CTA GGC GAC GGC CTA GAG GTC AGA GAC AAT AAA ATC ATT GTT AAG
 Pro Asn Leu Gly Asp Gly Leu Glu Val Arg Asp Asn Lys Ile Val Lys

3590 3600 3610 3620 3630
 CTG GGC GCG AAT CTT CGT TTT GAA AAC GGA GCC GTA ACC GCC GGC ACC GTT
 Leu Gly Ala Asn Leu Arg Phe Glu Asn Gly Ala Val Thr Ala Gly Thr Val

3640 3650 3660 3670 3680
 AAC CCT TCT GCG CCC GAG GCA CCA CCA ACT CTC ACT GCA GAA CCA CCC CTC
 Asn Pro Ser Ala Pro Glu Ala Pro Pro Thr Leu Thr Ala Glu Pro Pro Leu

3690 3700 3710 3720 3730
 CGA GCC TCC AAC TCC CAT CTT CAA CTG TCC CTA TCG GAG GGC TTG GTT GTG
 Arg Ala Ser Asn Ser His Leu Gln Leu Ser Leu Ser Glu Gly Leu Val Val

FIG. 7M

3740 3750 3760 3770 3780
CAT AAC AAC GCC CTT GCT CTC CAA CTG GGA GAC GGC ATG GAA GTA AAT CAG
His Asn Asn Ala Leu Ala Leu Gln Leu Gly Asp Gly Met Glu Val Asn Gln

3790 3800 3810 3820 3830
CAG GGA CTT ACT TTA AGA GTA GGC TCG GGT TTG CAA ATG CGT GAC GGC ATT
His Gly Leu Thr Leu Arg Val Gly Ser Gly Leu Gln Met Arg Asp Gly Ile

3840 3850 3860 3870 3880
TTA ACA GTT ACA CCC AGC GGC ACT CCT ATT GAG CCC AGA CTG ACT GCC CCA
Leu Thr Val Thr Pro Ser Gly Thr Pro Ile Glu Pro Arg Leu Thr Ala Pro

3890 3900 3910 3920 3930
CTG ACT CAG ACA GAG AAT GGA ATC GGG CTC GCT CTC GGC GCC GGC TTG GAA
Leu Thr Gln Thr Glu Asn Gly Ile Gly Leu Ala Leu Gly Ala Gly Leu Glu

3940 3950 3960 3970 3980 3990
TTA GAC GAG AGC GCG CTC CAA GTA AAA GTT GGG CCC GGC ATG CGC CTG AAC
Leu Asp Glu Ser Ala Leu Gln Val Lys Val Gly Pro Gly Met Arg Leu Asn

4000 4010 4020 4030 4040
CCT GTA GAA AAG TAT GTA ACC CTG CTC CTG GGT CCT GGC CTT AGT TTT GGG
Pro Val Glu Lys Tyr Val Thr Leu Leu Leu Gly Pro Gly Leu Ser Phe Gly

FIG. 7N

4050 4060 4070 4080 4090
CAG CCG GCC AAC AGG ACA AAT TAT GAT GTG CGC GTT TCT GTG GAG CCC CCC
Gln Pro Ala Asn Arg Thr Asn Tyr Asp Val Arg Val Ser Val Glu Pro Pro

4100 4110 4120 4130 4140
ATG GTT TTC GGA CAG CGT GGT CAG CTC ACA TTT TTA GTG GGT CAC GGA CTA
Met Val Phe Gly Gln Arg Gly Gln Leu Thr Phe Leu Val Gly His Gly Leu

4150 4160 4170 4180 4190
CAC ATT CAA AAT TCC AAA CTT CAG CTC AAT TTG GGA CAA GGC CTC AGA ACT
His Ile Gln Asn Ser Lys Leu Gln Leu Asn Leu Gly Gln Gly Leu Arg Thr

4200 4210 4220 4230 4240
GAC CCC GTC ACC AAC CAG CTG GAA GTG CCC CTC GGT CAA GGT TTG GAA ATT
Asp Pro Val Thr Asn Gln Leu Glu Val Pro Leu Gly Gln Gly Leu Glu Ile

4250 4260 4270 4280 4290
GCA GAC GAA TCC CAG GTT AGG GTT AAA TTG GGC GAT GGC CTG CAG TTT GAT
Ala Asp Glu Ser Gln Val Arg Val Lys Leu Gly Asp Gly Leu Gln Phe Asp

4300 4310 4320 4330 4340
TCA CAA GCT CGC ATC ACT ACC GCT CCT AAC ATG GTC ACT GAA ACT CTG TGG
Ser Gln Ala Arg Ile Thr Thr Ala Pro Asn Met Val Thr Glu Thr Leu Trp

FIG. 70

4350 4360 4370 4380 4390
ACC GGA ACA GGC AGT AAT GCT AAT GTT ACA TGG CGG GGC TAC ACT GCC CCC
Thr Gly Thr Gly Ser Asn Ala Asn Val Thr Trp Arg Gly Tyr Thr Ala Pro

4400 4410 4420 4430 4440
GGC AGC AAA CTC TTT TTG AGT CTC ACT CGG TTC AGC ACT GGT CTA GTT TTA
Gly Ser Lys Leu Phe Leu Ser Leu Thr Arg Phe Ser Thr Gly Leu Val Leu

4450 4460 4470 4480 4490 4500
GGA AAC ATG ACT ATT GAC AGC AAT GCA TCC TTT GGG CAA TAC ATT AAC GCG
Gly Asn Met Thr Ile Asp Ser Asn Ala Ser Phe Gly Gln Tyr Ile Asn Ala

4510 4520 4530 4540 4550
GGA CAC GAA CAG ATC GAA TGC TTT ATA TTG TTG GAC AAT CAG GGT AAC CTA
Gly His Glu Gln Ile Glu Cys Phe Ile Leu Leu Asp Asn Gln Gly Asn Leu

4560 4570 4580 4590 4600
AAA GAA GGA TCT AAC TTG CAA GGC ACT TGG GAA GTG AAG AAC AAC CCC TCT
Lys Glu Gly Ser Asn Leu Gln Gly Thr Trp Glu Val Lys Asn Asn Pro Ser

4610 4620 4630 4640 4650
GCT TCC AAA GCT GCT TTT TTG CCT TCC ACC GCC CTA TAC CCC ATC CTC AAC
Ala Ser Lys Ala Ala Phe Leu Pro Ser Thr Ala Leu Tyr Pro Ile Leu Asn

FIG. 7P

4660 4670 4680 4690 4700
GAA AGC CGA GGG AGT CTT CCT GGA AAA AAT CTT GTG GGC ATG CAA GCC ATA
Glu Ser Arg Gly Ser Leu Pro Gly Lys Asn Leu Val Gly Met Gln Ala Ile

4710 4720 4730 4740 4750
CTG GGA GGC GGC ACT TGC ACT GTG ATA GCC ACC CTC AAT GGC AGA CGC
Leu Gly Gly Gly Thr Cys Thr Val Ile Ala Thr Leu Asn Gly Arg Arg

4760 4770 4780 4790 4800
AGC AAC AAC TAT CCC GCG GGC CAG TCC ATA ATT TTC GTG TGG CAA GAA TTC
Ser Asn Asn Tyr Pro Ala Gly Gln Ser Ile Ile Phe Val Trp Gln Glu Phe

4810 4820 4830 4840 4850
AAC ACC ATA GCC CGC CAA CCT CTG AAC CAC TCT ACA CTT ACT TTT TCT TAC
Asn Thr Ile Ala Arg Gln Pro Leu Asn His Ser Thr Leu Thr Phe Ser Tyr

4860 4870 4880 4890 4900
TGG ACT TA AAT AAG TTG GAA ATA AAG AGT TAA ACT GAA TGT TTA AGT GCA
Trp Thr

4910 4920 4930 4940 4950
ACA GAC TTT TAT TGG TTT TGG CTC ACA ACA AAT TAC AAC AGC ATA GAC AAG

4960 4970 4980 4990 5000
TCA TAC CGG TCA AAC AAC ACA GGC TCT CGA AAA CGG GCT AAC CGC TCC AAG

FIG. 7Q

5010 5020 5030 5040 5050 5060
AAT CTG TCA CGC AGA CGA GCA AGT CCT AAA TGT TTT TTC ACT CTC TTC GGG

5070 5080 5090 5100
GCC AAG TTC AGC ATG TAT CGG ATT TTC TGC TTA CAC CTT T

FIG. 7R

Ad2	MSKEIPTPYMWSYQPQMGLAAGAAQDYSTRINYMSAGPHMISRVNGIRAH	50
BAV3	LIKQPVVGTTHV-----EMPRNEVLEQH	23
Ad2	RNRILLEQAAITTTTPRNNLNPRSWPAALVYQESPAPTTVVLPDAQAEVQ	100
BAV3	LTSHGAQIAGGG-----AAGDYFKSPTSARTLIPLTASCL-----RPDG	62
Ad2	MTNSGAQLAGGFRHRVRSPPGQGITHLKIRGRGIQLNDESVSSSLGLRPDG	150
BAV3	VFQLGGGSRSSFNPLQTDFAFHALPSRPRHGGIGSRQFVEEFVPAVYLN	112
Ad2	TFQIGGAGRSSFTPRQAILTLQTSSEPRSGGIGTLQFIEEFVPSVYFNP	200
BAV3	YSGPPDSYPDQFIRHYNVYSNSVSGYS	139
Ad2	FSGPPGHYPDQFIPNFDVAVKDSADGYD	227

FIG. 8A

BAV3	M-----EPDGVHAEQQFILNQISCANTALQRQREELASLVMLHACKRGL	77
Ad5	MTDTLDLEMDGIITEQRL--ERRRAAAEQQRMNQELQDMVNLHQCKRGI	48
BAV3	FCPVKTYKLSLNASASEHSLHFEKSPSRFTLVNTHAGASVRVALHHQGAS	127
Ad5	FCLVKQAKVTYDSNTTGHRLSYKLPTRQKLVVMVGEKPITITQHSVETE	98
BAV3	GSIRCSCSHAECPLVLLKTLCAFNFLD	154
Ad5	GCIHSPCQGPEDLCTLIKTLCLGLKDLIPFN	128

FIG. 8B

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BAV3      - MKRSVPQD--FNLVYPYKAKR-----PNIMPPFFDRNGFVENQEATLAML -43
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - MKRARPSEDTFNPVYPYDTETGPPTVPFLTTPPFVSPNGFQESPPGVLSLR -50

BAV3      - VEKPLTFDKE-GALTIGVGRGIRINPAGLLETNDLASAVFPPLASDEAGN -92
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - VSEPL--DTSHGMLALKMGSGLTLDKAGNLTSQNVTTV----- -86

BAV3      - VTLNMSDGLYTKDNKLAVKVGPGLSLDSNNALQVHTGDGLTVTDDKVSLN -142
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - -----TQPLKKTksNISLDTsAPLTI-TSGALTvATTAPLIvTSGALsvQ -130

BAV3      - TQAPLSTTSAGLSLLLGP SLHLGEEERLTvNTGAGLQISNNALAVKVGSg -192
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - SQAPLT-----VQDSKLSIATKGPITVSDGKLALQTSAP -164

BAV3      - ITVDAQNQLAASLG DGLES RDNKTvVKAGPGLTITNQALTvATGNGLQVN -242
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - LSGSDSDTLTVT-----ASPPLTTATGS-LGIN -191

BAV3      - PEGQLQLNITAGQGLNFANNSLAVELGSGLHFPPGQNQVSLYPGDGIDIR -292
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - MEDPIYVN-----NGKIGIKISGPLQVAQ----- -215

BAV3      - DNRVTVPAGPGLRMLNHQLAVASGDGLEVHSDTLRLKLSHGLTFENGAVR -342
          : : : : : : : : : : : : : : : : : : : : : : : : : :
Ad2        - -----NSDTLTVVTGPGVTVEQNSLR -236

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FIG. 8C-1

BAV3 - AKLGPGGLGTDDSGRSVVRTGRGLRVANGQVQIFSGRGTAIGTDSSTLTNI - 392
 Ad2 - TKVAGAIGYDSSNNMEIKTGGGMRINNLL--LILDVDYPFDAQTKLRRLKL - 284
 BAV3 - RAPLQFSGPALTASLQSGSPITYNSNNGTFGLSIGPGMWVDQNRLQVNPG - 442
 Ad2 - -----GQGPLYINASHN-----LDINYN - 302
 BAV3 - AGLVFQGNLVPNLADPLAISDSKISLSLGPGLTQASNALTLSLGNGLEF - 492
 Ad2 - RGLYL-----FNASNNTKKLEVSIIKSS-----GLNF - 329
 BAV3 - SNQAVAIKAGRGLRFESSQALESSTLVGNGLTLTDTVIRPNLGDGLEVR - 542
 Ad2 - DNTAIAINAGKGLEFDTNT----- - 348
 BAV3 - DNKIIIVKLGANLRFENGAVTAGTVNPSAPEAPPTLTAEPPLRASNHLQL - 592
 Ad2 - ----- - 348
 BAV3 - SLSEGLVVHNNALALQLGDGMEVNQHGLTLRVGSGLQMRDGILTVTPSGT - 642
 Ad2 - -----SESPDIN--PIKTKIGSGID-----YNENGA - 372
 BAV3 - PIEPRLTAPLTQTENGIGLALGAGLELDESALQVKVGPGMRLNPVEKYVT - 692
 Ad2 - MIT-----KLGAGLSFDNSG----- - 387

FIG. 8C-2

BAV3 - LLLGPGLSFGQPANRTNYDVRVSVEPPMVFGQRGQLTFLVGHGLHIQNSK - 742
 Ad2 - -----AITIG-----NKNDKLTLTWTPDPSP-----NCR - 412
 BAV3 - LQLNLGQGLRTDPVTNQLEVPLQGGLIADDESQVRVKLGDGLQFDSQARI - 792
 Ad2 - IHSD-----NDCKFTLVLT---KCGSQVLA - 434
 BAV3 - TTAPNMVTETLWTGTGSNANVTWRGYTAPGSKLFLSLTRFSTGLVLGNMT - 842
 Ad2 - TVAALAVSGDLSSMTGTVASVS-----IFLRFDQ--NGVLMENSS - 472
 BAV3 - IDSNASFGQYINAGHEQIECFILLDNQGNLKEGSNLQGTWEVKNNPSASK - 892
 Ad2 - LKKHY-----WNFRNGNS-----TNANPYTNA - 494
 BAV3 - AAFLPSTALYPILNESRGSLPGKNLVGMQAILGGGTCTVIA--TLNGRRS - 941
 Ad2 - VGFMPLNLLAYP---KTQSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSE - 541
 BAV3 - NNYPAGQSII---FVWQ--EFNTIARQPLNHSTLTFSYWT - 976
 Ad2 - STETSEVSTYSMSFTWSWESGKYTTTETFATNSYTFYSYIAQE - 582

FIG. 8C-3



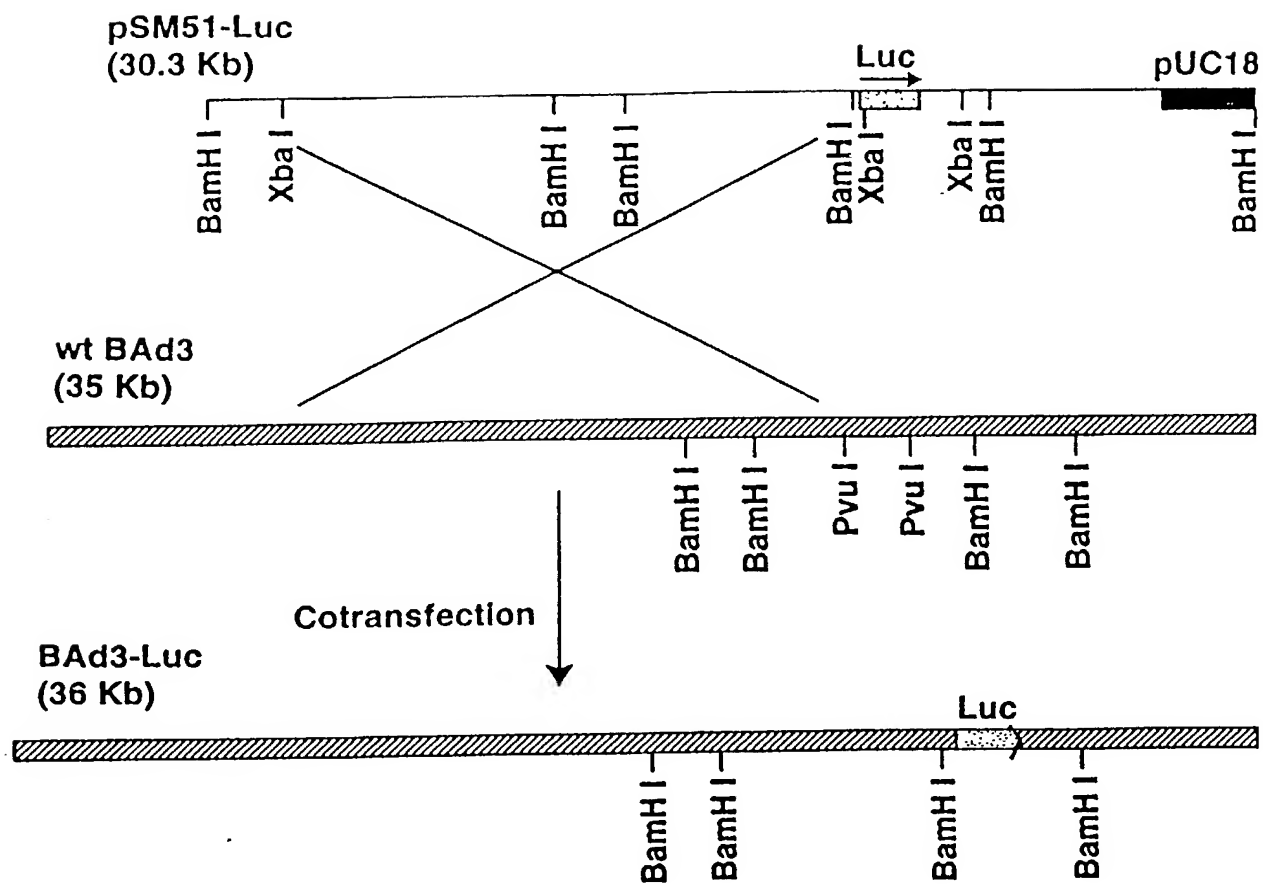
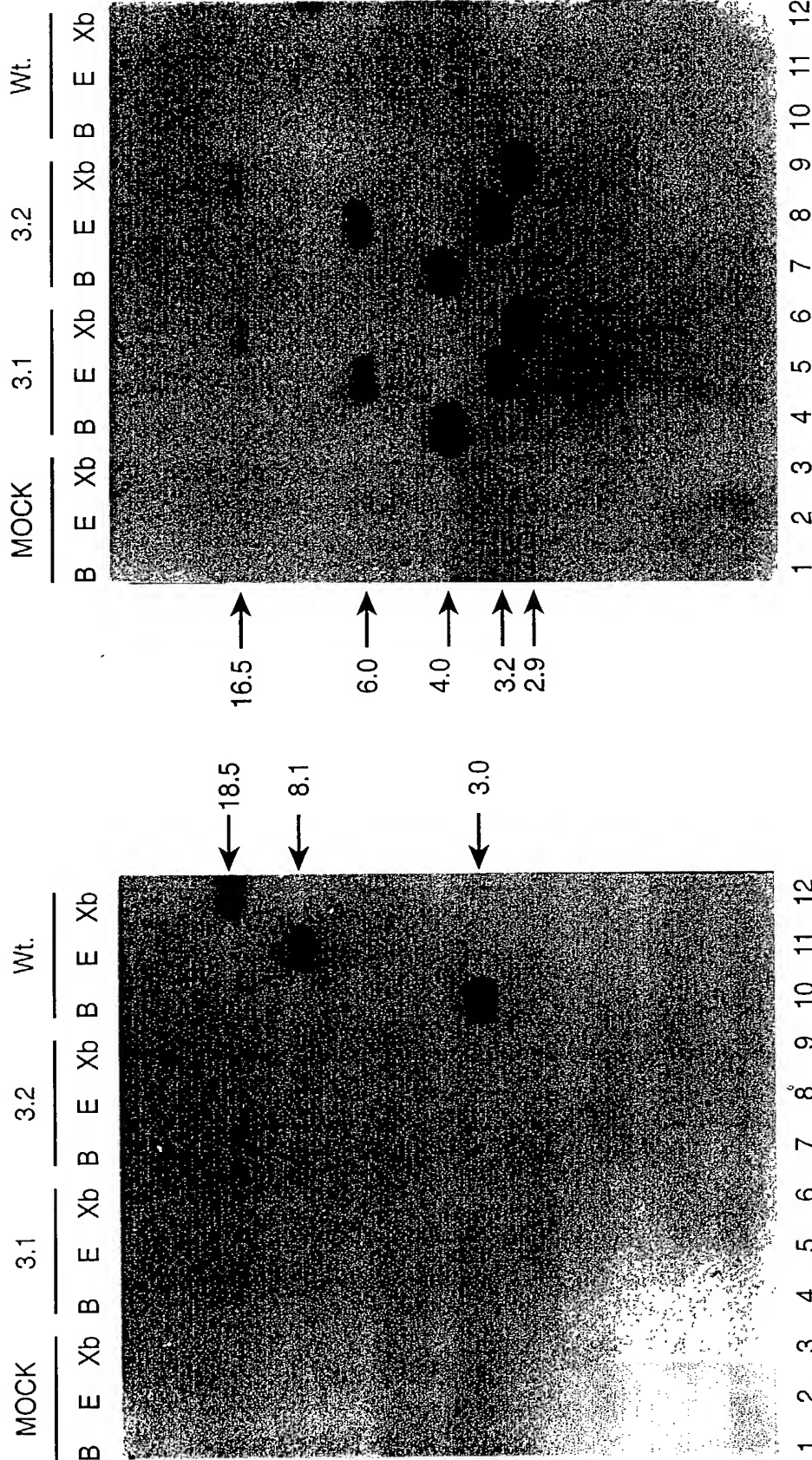


FIG. 10



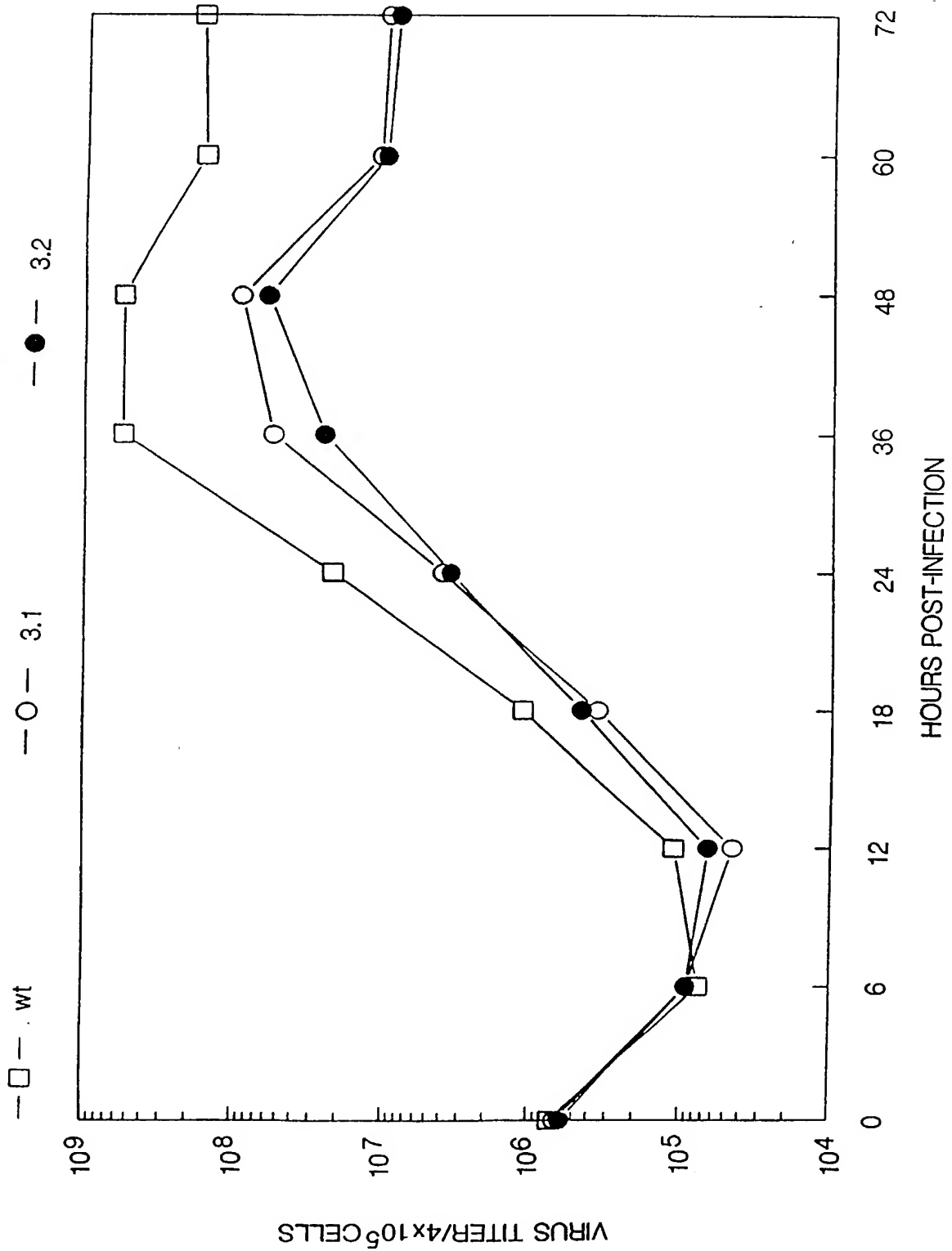


FIG. 12

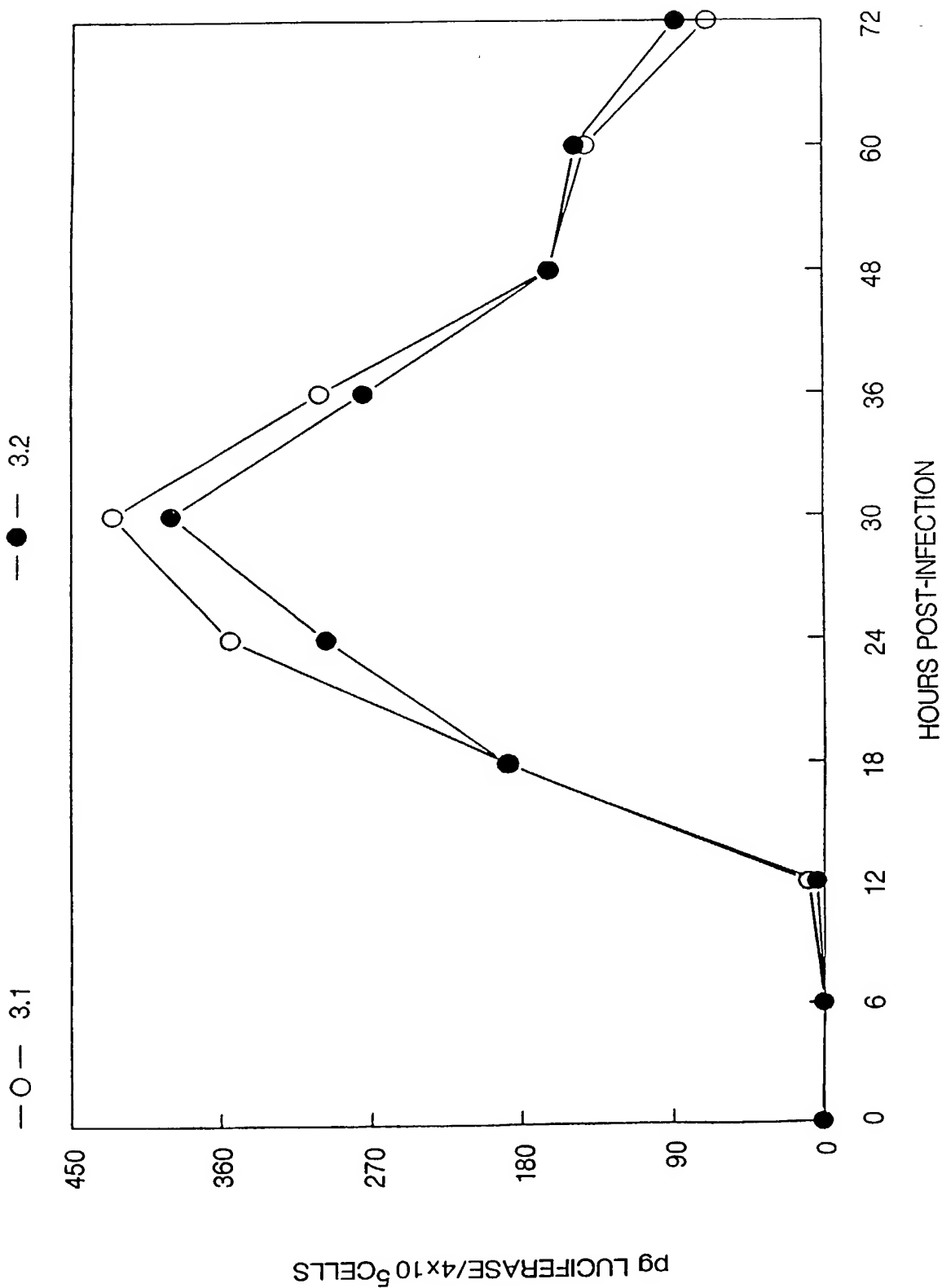


FIG. 13

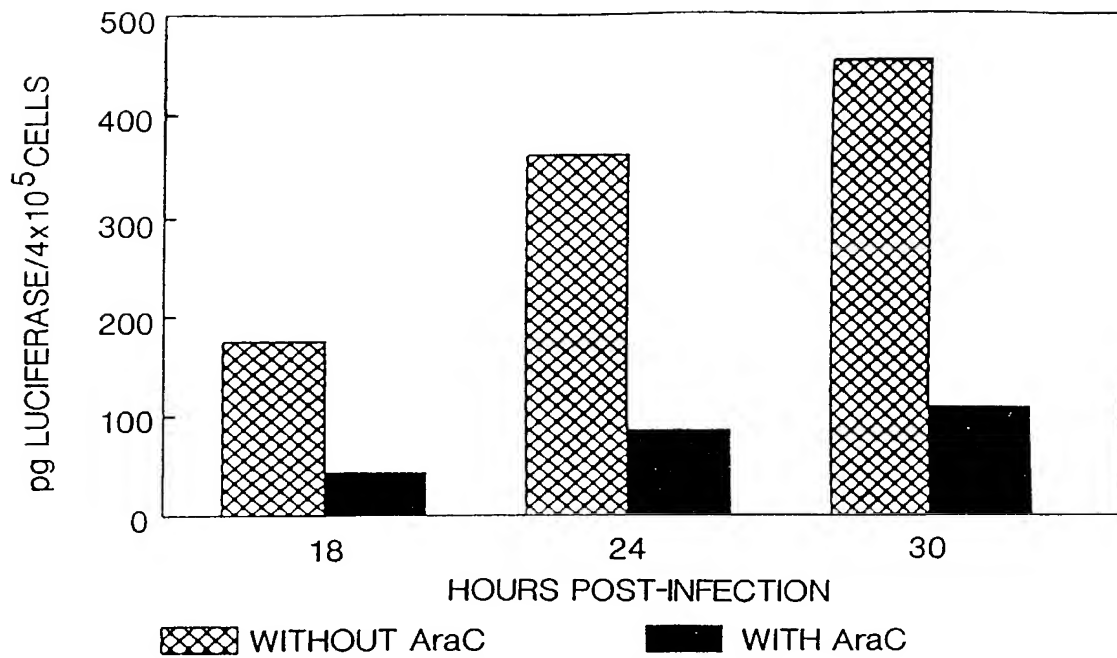


FIG. 14A

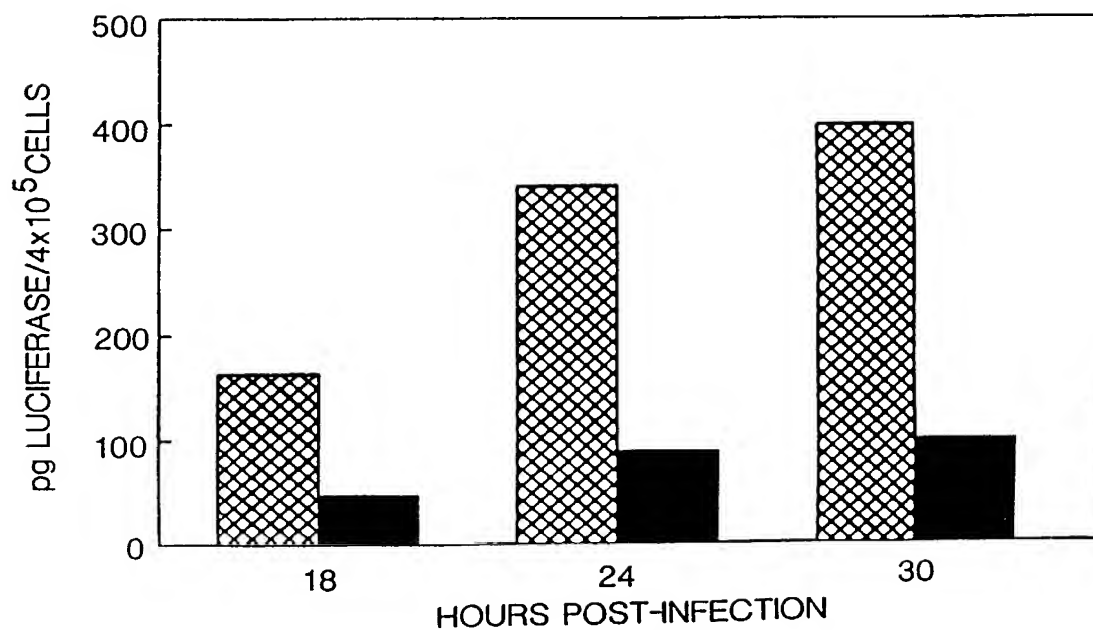


FIG. 14B

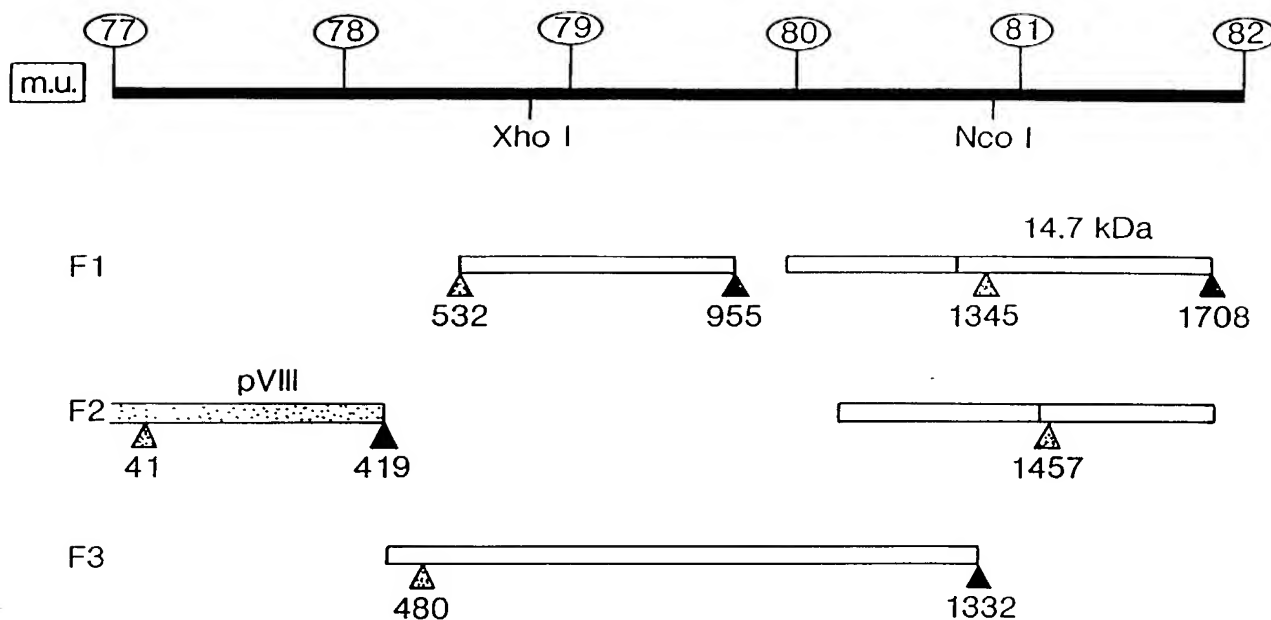


FIG. 15A

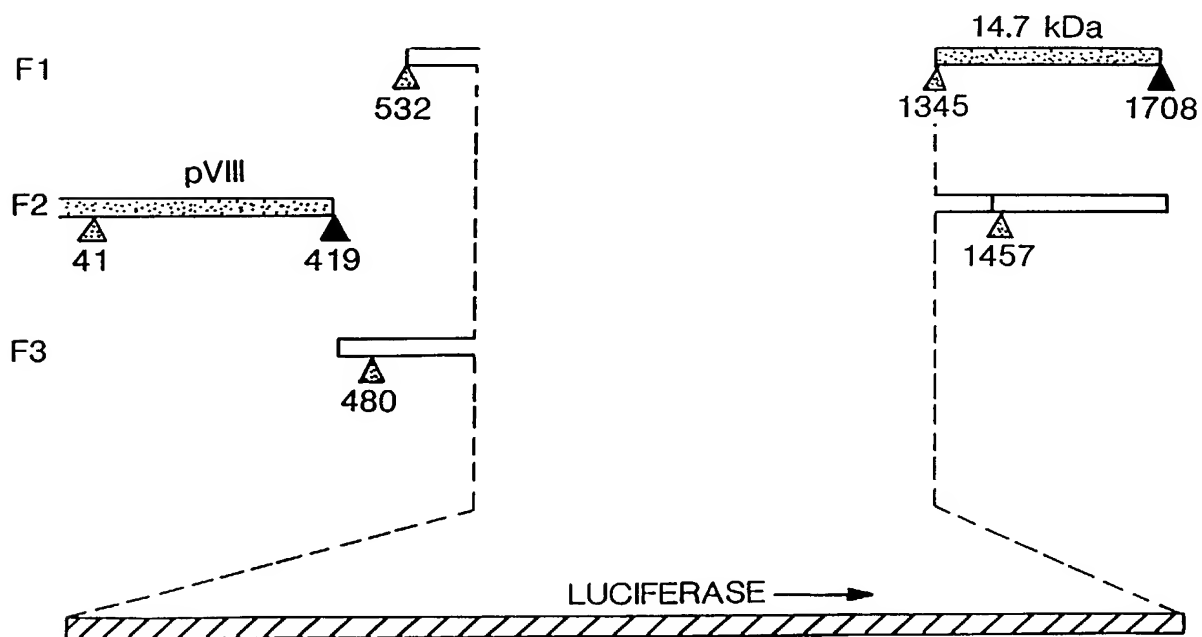


FIG. 15B

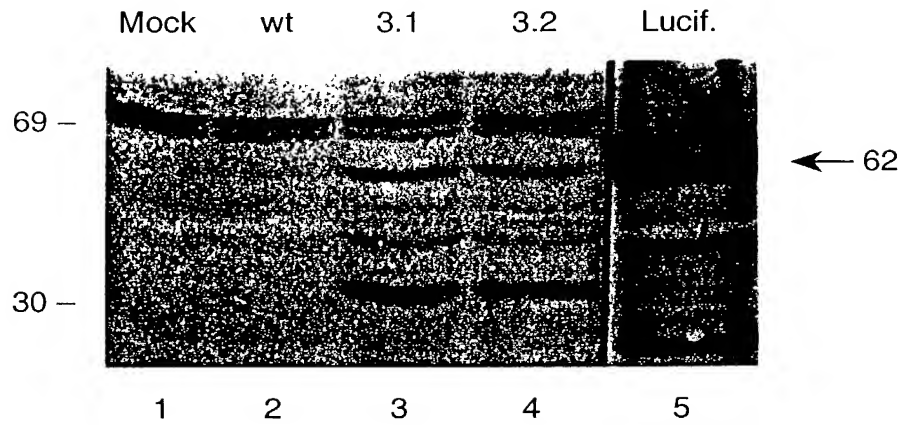


FIG. 16

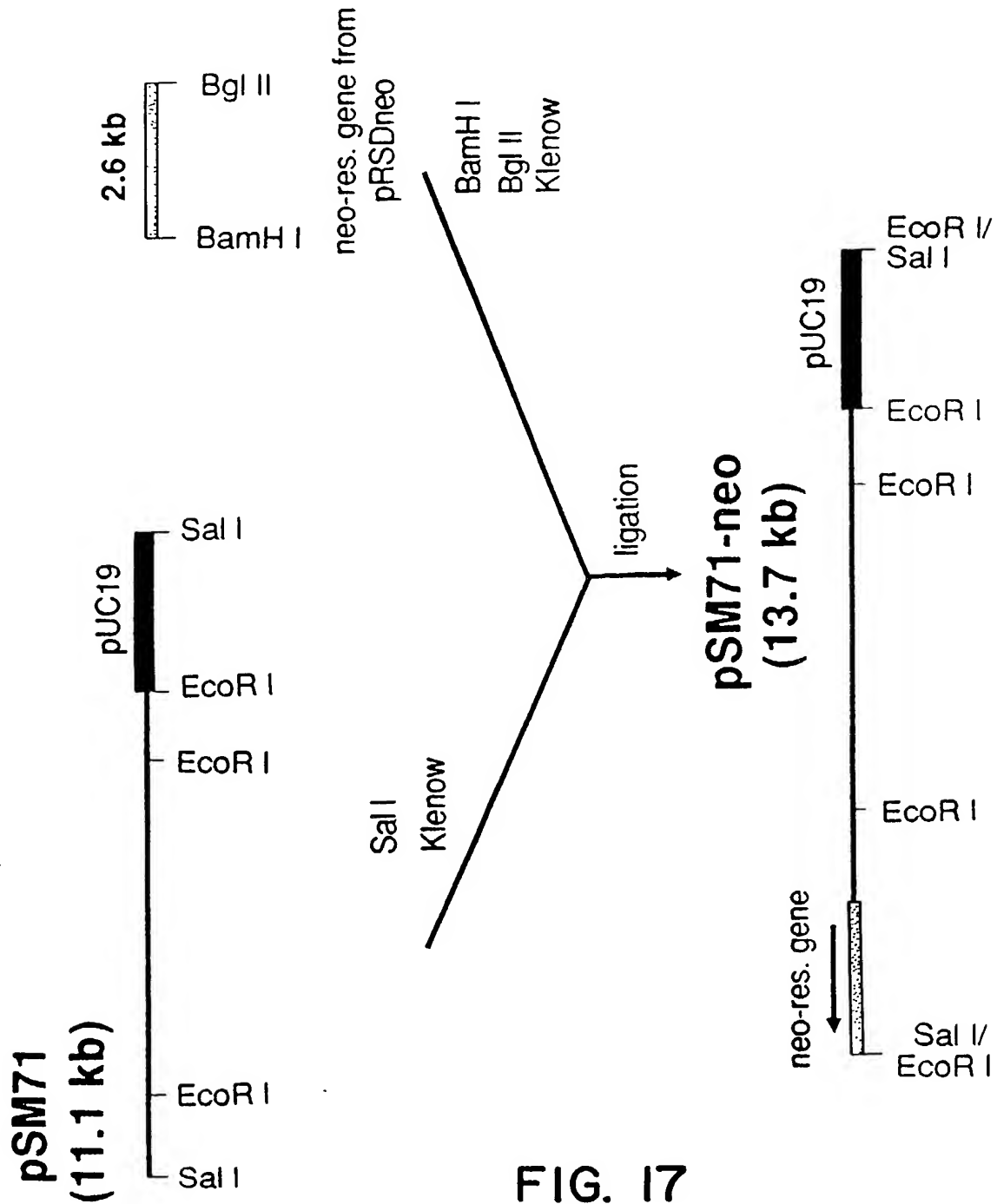


FIG. 17

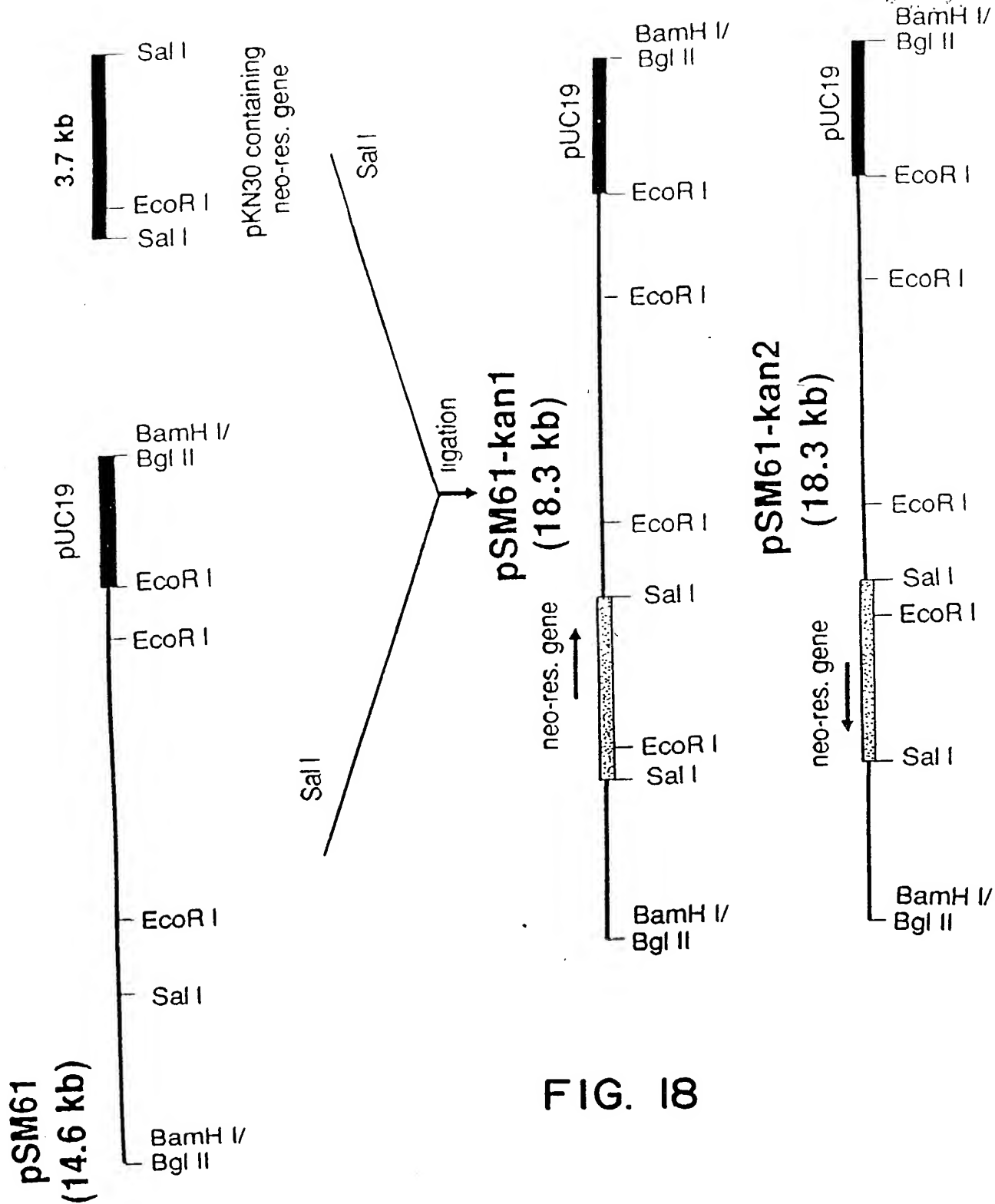


FIG. 18

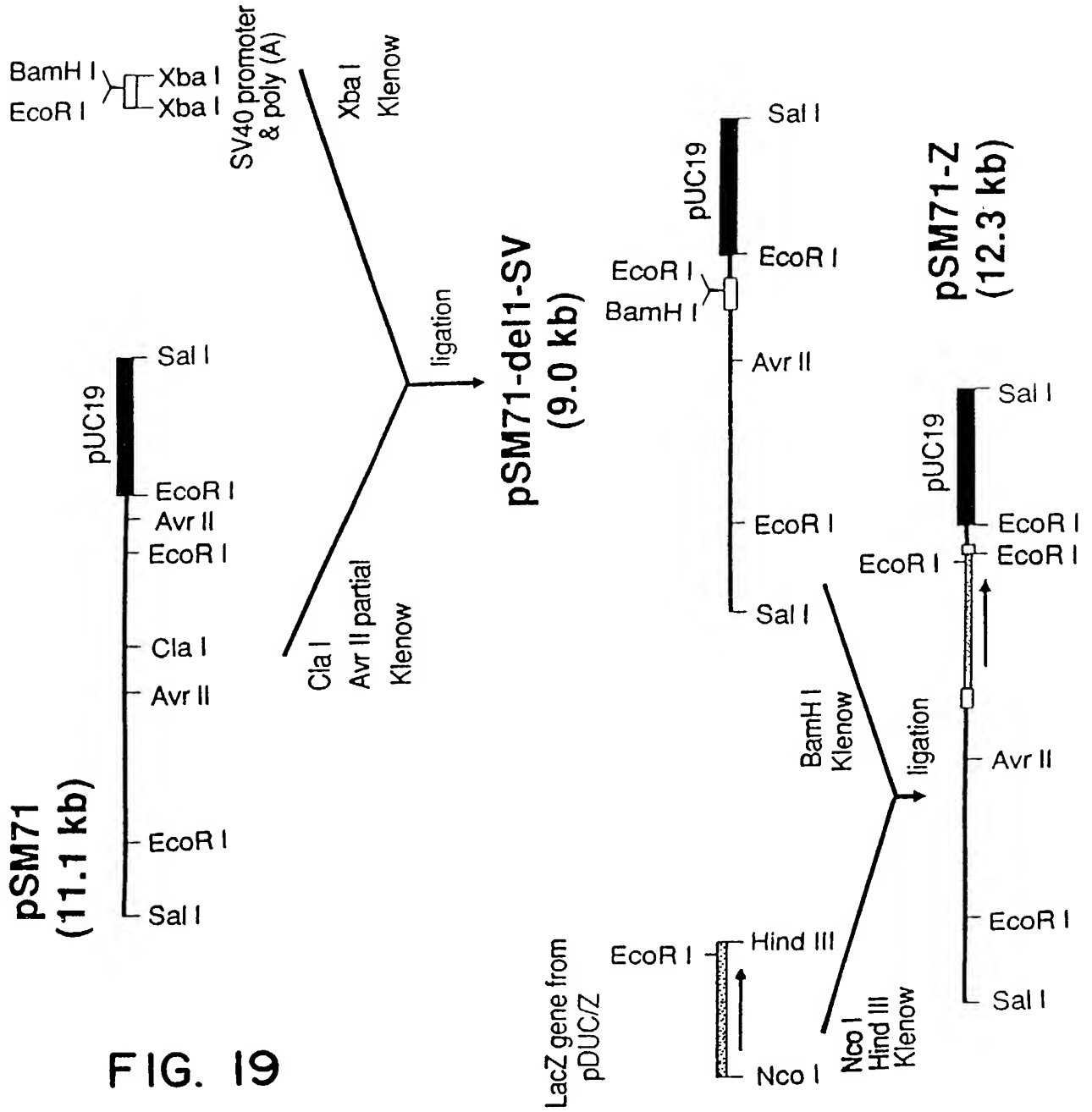


FIG. 19